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Major Article

Distribution of the bla_{OXA}, bla_{VEB-1}, and bla_{GES-1} genes and resistance patterns of ESBL-producing *Pseudomonas aeruginosa* isolated from hospitals in Tehran and Qazvin, Iran

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Abstract

Introduction: *Pseudomonas aeruginosa* is one of the most common nosocomial pathogens. The emergence of extended spectrum β-lactamases (ESBLs) has been increasingly reported as a major clinical concern worldwide. The main aim of the present study was to determine the distribution of bla_{OXA}, $bla_{PER-1,}$ $bla_{VEB-1,}$ and bla_{GES-1} genes among ESBL-producing *P. aeruginosa* isolated from two distinct provinces in Iran. **Methods:** In this study, a total of 75 (27.5%) ESBL-producing isolates were identified from 273 *P. aeruginosa* isolates collected from patients in Qazvin and Tehran. Phenotypic detection of ESBLs and antimicrobial susceptibility testing were performed according to the Clinical and Laboratory Standards Institute guidelines. PCR and sequencing were employed to detect bla_{OXA-1}, bla_{OXA}, $bla_{GES-1,}$ bla_{PER-1}, and bla_{VEB-1} genes. Isolate genetic relationships were evaluated by repetitive extragenic palindromic sequence-based PCR (REP-PCR). **Results:** In total, 59 (78.7%) of the ESBL-producing isolates showed multidrug resistance. The highest rates of susceptibility were observed against colistin (75 isolates, 100%) and polymyxin B (75, 100%) followed by amikacin (44, 58.7%), and piperacillin-tazobactam (40, 53.3%). The bla_{OXA-1} (37.3%) gene was the most common of the genes investigated, followed by bla_{OXA-4} (32%), bla_{GES-1} (16%), and bla_{VEB-1} (13.3%). REP-PCR identified three different genotypes: types A (89.3%), B (6.7%), and C (4%). **Conclusions:** We found a significant presence of bla_{OXA-1}, bla_{OXA-4}, $bla_{GES-1,}$ and bla_{VEB-1} genes among *P. aeruginosa* isolates, highlighting the need for suitable infection control strategies to effectively treat patients and prevent the further distribution of these resistant organisms.

Keywords: *Pseudomonas aeruginosa.* bla_{OXA}. bla_{VEB-1}. bla_{GES-1}. Repetitive extragenic palindromic sequence-based PCR.

INTRODUCTION

Pseudomonas aeruginosa is the most frequent bacterial species associated with infections such as urinary tract infections, respiratory infections, dermatitis, soft tissue infections, gastrointestinal infections, and a variety of systemic infections, particularly in patients with severe burns, cancer, and acquired immunodeficiency syndrome (AIDS)[1,2]. Infections caused by *P. aeruginosa* develop intrinsically and may exhibit acquired resistance against various commonly prescribed antimicrobial drugs. In addition, infections caused by this organism are often difficult to treat, as they eventually reveal the emergence of multi-drug resistant *Pseudomonas aeruginosa* (MDRPA) isolates[3]. Nosocomial infection with MDRPA is a serious growing concern worldwide and is associated with higher morbidity, mortality, and cost of therapy[4].

There are several mechanisms for the emergence of resistance to β-lactam antibiotics, with extended-spectrum β-lactamases (ESBLs) among the leading causes[5,6]. These enzymes are plasmid-encoded β-lactamases commonly found in *Klebsiella pneumoniae* and *Escherichia coli* and also observed in other clinical isolates of Enterobacteriaceae and *Pseudomonas*[7-9]. It is clear that the TEM (temoniera), SHV (sulfhydryl-variable), and CTX-M (cefotaximase) proteins are the principal types of ESBLs among clinically important Enterobacteriaceae species; however, the presence of less-studied types of ESBLs, including OXA (oxacillinase), VEB (Vietnamese extended spectrum β-lactamase), PER (Pseudomonas extended resistant), and GES (Guyana extended spectrum β-lactamase), has been reported in other bacterial species[10,11]. Recent studies have indicated that the dissemination of genes that encode ESBLs may play an important role in the spread of antibiotic resistance and may complicate the treatment of infections caused by *P. aeruginosa*

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